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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/666,642	09/18/2003	Cai-Zhong Jiang	MBI-0054	9792

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EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 10/11/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/666,642	JIANG ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *27 July 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *21-40* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *21-40* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *18 September 2003* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *8/5/2005*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 21-40 are pending.

2. Applicant's election without traverse of Group I, claims 1-20, including SEQ ID NO:193 encoding SEQ ID NO:194 in the reply filed on 7/27/2005 is acknowledged.

Claims 1-20 have been canceled.

Claims 21-40 have been newly added and are drawn to the elected invention.

3. Claims 21-40, including SEQ ID NO:193 encoding SEQ ID NO:194 are examined in the present office action.

Specification

4. The Specification is objected to because the drawings are not referred to properly. If, for example, the drawings show Figures 3A and 3B, then the Brief Description of the Drawings should recite "Figures 3A-3B", instead of "Figure 3" or "Figure 3A". Applicant is requested to check over the Brief Description of the Drawings for compliance. Correction is requested.

Written Description

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claims 21-40 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one

skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a transgenic plant transformed with a polynucleotide encoding a polypeptide having a conserved domain that has at least 70% sequence identity to the amino acid coordinates 111-164 of SEQ ID NO:194, or a method for producing a transgenic plant having an altered trait or a method for increasing the tolerance of a plant to an abiotic stress comprising introducing a polynucleotide encoding a polypeptide having a conserved domain that has at least 70%, 75% or 80% sequence identity to the amino acid coordinates 111-164 of SEQ ID NO:194.

Applicants disclose that polynucleotides encoding the polypeptides of the invention were identified in the Arabidopsis thaliana GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specific sequence strings corresponding to sequence motifs present in families of known transcription factors. Additional polynucleotides of the invention were identified by screening Arabidopsis thaliana and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions (page 33, lines 26-35; paragraph bridging pages 33-34). Applicants disclose SEQ ID NO:193 encoding SEQ ID NO:194. Said sequence is designated as G1274 and is a member of the WRKY family of transcription factors. The gene corresponds to WRKY51 (At5g64810). Applicants disclose that no information is available about the function of G1274 (page 409, lines 29-32).

Applicants have not fulfilled the written description requirement for the claimed genus of proteins comprising the conserved domain comprising amino acid coordinates 111-164 of SEQ

ID NO:194. Applicants do not identify essential regions of proteins comprising the conserved domain comprising amino acid coordinates 111-164 of SEQ ID NO:194, nor do Applicants describe any polynucleotide sequences that encode a protein comprising a conserved domain that has at least 70% sequence identity to amino acid coordinates 111-164 of SEQ ID NO:194 and has the same function and activity as the protein G1274 of SEQ ID NO:194.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of polynucleotide sequences encoding a G1274 protein falling within the scope of the claimed genus of polynucleotides which encode a protein comprising a conserved domain that has at least 70% sequence identity to amino acid coordinates 111-164 of SEQ ID NO:194. Applicants only describe a single sequence of SEQ ID NO:193 encoding SEQ ID NO:194. Furthermore, Applicants fail to describe structural features

common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of disclosure about other domains that are required along with the conserved domain comprising amino acid coordinates 111-164 of SEQ ID NO:194, it remains unclear what features identify a protein with the same activity and function as Applicants' G1274 of SEQ ID NO:194. Since the genus of proteins comprising the conserved domain comprising amino acid coordinates 111-164 of SEQ ID NO:194 has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Enablement

6. Claims 21-40 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are drawn to a transgenic plant transformed with a polynucleotide encoding a polypeptide having a conserved domain that has at least 70% sequence identity to the amino acid coordinates 111-164 of SEQ ID NO:194, or a method for producing a transgenic plant having an altered trait or a method for increasing the tolerance of a plant to an abiotic stress comprising introducing a polynucleotide encoding a polypeptide having a conserved domain that has at least 70%, 75% or 80% sequence identity to the amino acid coordinates 111-164 of SEQ ID NO:194, wherein the altered trait is selected from the group consisting of greater tolerance to cold during germination, greater tolerance to cold during growth, greater tolerance to drought, greater tolerance to nitrogen limitation, larger leaves, and greater biomass than the wild-type plant and wherein the abiotic stress is selected from the group consisting of cold stress during germination, cold stress during growth, drought stress and nitrogen limitation, or wherein the polypeptide comprises a DNA-binding domain combined with a GAL4 activation domain.

Applicants disclose that polynucleotides encoding the polypeptides of the invention were identified in the Arabidopsis thaliana GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specific sequence strings corresponding to sequence motifs present in families of known transcription factors. Additional polynucleotides of the invention were identified by screening Arabidopsis thaliana and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions (page 33, lines 26-35; paragraph bridging pages 33-34). Applicants disclose SEQ ID NO:193 encoding SEQ ID NO:194. Said sequence is designated as G1274 and is a member of the WRKY family of transcription factors. The gene corresponds to WRKY51 (At5g64810).

Applicants disclose that no information is available about the function of G1274 (page 409, lines 29-32). Applicants disclose that Arabidopsis plants transformed with a nucleic acid encoding the G1274 polypeptide of SEQ ID NO:194 operably linked to the 35S promoter produced plants that grew larger and greener in a cold germination assay compared to control plants (page 410, lines10-12). Applicants disclose that said Arabidopsis plants comprising the 35S::G1274 construct fared much better after a period of water deprivation than control plants. The 35S::G1274 plants fully recovered after being watered whereas control plants did not recover (page 410, lines 13-18). The 35S::G1274 transgenic plants were more tolerant to chilling compared to control plants in both germination as well as seedling growth assays. The 35S::G1274 overexpression plants were significantly greener and larger than control plants in a soil-based drought assay (page 410, lines19-22). Applicants also disclose that overexpression of G1274 produced alterations in leaf morphology and inflorescence architecture (page 410, lines 23-26).

Applicants' claims are drawn to a conserved domain of the WRKY family of transcription factors, and it has not been disclosed that any member of the family having the claimed domain will also produce the desired results when transformed into a plant. The state-of-the-art teach overexpressing a WRKY transcription factor in a plant produces unexpected results. Miao et al (2004, Plant Molecular Biology 55:853-867) state "Arabidopsis WRKY proteins comprise a family of plant specific zinc-finger-type transcription factors involved in the regulation of gene expression during pathogen defense, wounding, trichome development and senescence (page 853, abstract). Miao et al teach overexpressing the transcription factor, WRKY53, which is a member of the WRKY family of transcription factors, in Arabidopsis

caused plants to flower early and the senescence of the whole plant was visible two weeks earlier compared to wild-type plants (page 861, left column). Miao et al disclose that in Arabidopsis plants overexpressing WRKY53, five other member of the WRKY protein family were strongly expressed, but were not detectable in the respective wild-type plants (page 861, right column, 2nd full paragraph). In addition, Expression profiling using Affymetrix genome arrays (approximately 22,000 genes) revealed that overexpression of WRKY53 leads to changes in mRNA levels of 1772 genes which showed changes in expression of at least 4-fold (page 861, right column, last sentence).

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that are 70% sequence identical to amino acid coordinates 111-164 of SEQ ID NO:194 will encode a protein with the same activity as amino acid coordinates 111-164 of SEQ ID NO:194. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Re: claim 30 is drawn to a method as stated above, wherein the polypeptide comprises any DNA-binding domain combined with any GAL4 activation domain. Applicants have not

provided guidance by way of disclosure or example, for one of skill in the art, to select any DNA-binding domain and to combine it with any GAL4 activation domain, for use in the claimed method. Applicants have not shown that substituting the endogenous DNA-binding domain and endogenous activation domain with any DNA-binding binding domain and any GAL4 activation domain, will produce the expected result. Applicants have not disclosed that using any DNA binding domain that facilitates binding to any consensus sequence, will also produce the desired results. The state-of-the-art teaches that transforming a plant with any transcription factor produces unexpected results. It is known in the art, that transcription factors have DNA-binding domains and activation domains. Yang et al (2001, PNAS 98(20):11438-11443) teach transgenic rice plants constitutively expressing the REB transcription factor produced mutant plants that were sterile. Yang et al state "Presumably, this aberrant phenotype is because of the constitutive expression of the transcriptional activator REB in all plant cells, causing disturbances of the normal gene expression program during rice development" (page 11443, left column, bottom paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments encoding amino acid coordinates 111-164 of SEQ ID NO:194 as probes or by designing primers to undisclosed regions of amino acid coordinates 111-

164 of SEQ ID NO:194 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those, if any, that when over-expressed produce a plant with the desired phenotype and wherein the polypeptide comprises a conserved domain that has at least 70% sequence identity to amino acid coordinates 111-164 of SEQ ID NO:194.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

7. No claims are allowed.

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones can be reached on 571-272-0745. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
September 30, 2005